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MDYGGALSAVGRELLFVTNPVVNGSVLPEDQCYCAGWIE
SRGTNGAQTASNVLQWLAAGFSILLMFYAYQTWKSTCGWE
EIYVCAIEMVKVILEFFFEFKNPSMLYLATGHRVQWLRYAEWL
LTCPVILHLSNLTGLSNDYSRRTMGLLVSDIGTIVWGATSAMA
TGYVKVIFFLCLGCLCYGANTFFHAAKAYIEGYHTVPKGRQRQV
VTGMAWLFFVSWGMFPILFILGPEGFVLSVYGSTVGHITIIL
MSKNCWGLLGHYLRVLIHEHILIHGDIRKTTKLNIGGTEIEVETL
VEDEAEAGAVNKGTKYASRESFLVMRDKMKEKGIDVRASL
DNSKEVEQEQAARAAMMMNGNGMGMGMGMNGMNGMG
GMNGMAGGAKPGLLETPQLQPGRVILAVPDISMVDFREQFA
QLSVTYELVPALGADNTLALVTQAQNLGGVDFVLIHPEFLRDR
SSTSILSRLRGAGQRVAAFGWAQLGPMRDLIESANLDGWLE
GPSFGQGILPAHIVALVAKMQQMRKMQQMQQIGMMTGGMN
GMGGGMGGGMNGMGGGNGMNNMGNGMGGGMGNGMG
NGMNGMGGGNGMNNMGNGMAGNGMGGGMGGNGMG
SMNGMSSGVVANVTPSAAGGMGGMNGGMAAPQSPGMN
GGRLGTNPLFNAAPSPLSSQLGAEAGMGSMMGGMGGMSGM
GGMGGMGGMGGAGAATTQAAGGNAEAEMLQNLNMNEINRL
KRELGE (SEQ ID NO:2)

Fig 1B

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MlptavegvsqAQITGRPEWIWLALGTALMGLGTLYFLVKMGVS
DPDAKKFYAITTLVPAIAFTMYLSMLGYGLTMVPFGGEQNP
YWAYADWLFTTPLLLLDLALLVDADQGTILALVGADGIMIGT
GLVGALTKVYSYRFVWWAISTAAML YILYVLFFGFTSKAESMR
PEVASTFKVLRNVTVVLWSAYPVWWLIGSEGAGIVPLNIETLLF
MVLDVSAKVGFGILLRSRAIFGEAEAPEPSAGDGAAATSD
(SEQ ID NO: 3)

Fig. 1C

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Chop1..MSRRPWLLALALAVALAAGSAGASTGSDATVPVATQDGPDIYVHRAHEEM FQTSYTLEN 60
 Chop2.....NGSVL-VED-CCYCAGWIER-.....MDYGGALS AVGHEILFVTNPVV 23
 Bop.....M

Chop1..NGSVICINNGOCFCIALKKN--GMAEKLHANIOMITFALSAPCLMEYGIOTWASTC 118
 Chop2..NGSVL-VED-CCYCAGWIER- -GNGAOTASNVLOMLAAGFSILINMYAYGTOKSIC 79
 Bop..LPTAVEGVSOAQITGRPEWIIWLALETALMG GTLYFLVKGNVSDPDAKKFYAI TLVPA 51

Chop1..GHELYATIERIETIYYHE DEPAVI SSN KTVMLRVAEMLTICQVILHESNAT 178
 Chop2..GHELYCALINAVVLEFFFKNE SMLLAT HRVOM RVAEMLTICQVILHESNAT 139
 Bop..IAFTMY---LSNLLGYGLTMVPEGGEQ-----NPIYCARADIEFT LLDLA-LL 100

Chop1..SIANDYNKPTN-GIAYSDDIGTAVETTAISKGV- -KVFILMGLCAGIIEFNAA-KVY 235
 Chop2..GLSNDSPRETM-GELVSDIGTAVAGALS MATCAV- -KVFILMGLCAGIIEFNAA-KAY 196
 Bop..V-DAL-Q-GHILAIVGADGIMGTCLVGTITVSYEFVWVAISTAAMLILYVLFEGFT 157

Fig. 1D

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* * * * *
 Chop1.. IFPAHTVPKICICRDLRYLETLVVCSWAMEVGFILGIEGEGCHINQFNSAIAFAILDIRAS 295
 Chop2.. IGHHIVPKRCRQVVTGMWLFVSWGNEILFIIGCEGHALISVYGSTVGTITIDIMS 256
 Bop.. SKIESMREEV--ASTFKVERNVIVLWSAFWVIIISEGAGIVPLNIEITLLFMVLDISA 215
 #
 Chop1.. KQATSMMCHEIRVKIHDLLYEDIRKQVNVAGQOMVEVEMHEDDDETQKVP-HAY 354
 Chop2.. KRCWGLIGHYERVLIIHDLIRKTTILNIGETIEVETLVEDFAEAGAVNKGTIG 316
 Bop.. KVGEGLI--LINSRAIFGEAEAPEPSAGDGA-AETSD (Seq ID No. 3)
 Chop1.. ANRDSFIIMFURLKQKFETESGADGDPNGDAFANEAGKKPGMEMCKMTGCMGMSMGAG 414
 Chop2.. ASKEISLVMMKMKKIKIDVRSSLENSKEVEQEQARRAMMMNGNGMGEMGNGMNG 376
 Chop1.. GNATIDS-----ENHIAVETLSMVQVETKQETPFAVILIVFAGAEET 459
 Chop2.. GMNGMAGGAKPGLETPQLQPEEMILAVEDLSMVDETREQFAQISVTYELHAICAIDH 436
 Chop1.. IQVQQASLTCGCDRVIMHETFDDRSPGLPKRMGCGQAPATGMAIGPVRDLINGS 519
 Chop2.. IAVITQALQMLGGVDEVALIHETFDDRSSSTLSRRGAGQVFAVFGNAQLCEMRDLISA 496
 Chop1.. GVDGWLEGSPGACINQOALVAINRMQAKRMGMG-----GNGMGMGCGNGM 568
 Chop2.. NLDGWLEGSPGQGLPAHIVAKQNRQQOQOIGMTGTGMNCGGCGGCGNGNG 556

Fig. 1D (continued)

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Chop1.. GMAEAGG-TAPSPNACGTGGTCT---ASNG-----AVMSMGCMQMPQQAMP--AMSPM 616
Chop2.. CGENNNYNGMGCGGNCGNMNGCGEGNGMNWNGNVMAGNMGVGGMGGNGFSGS 616

Chop1..TTQPS..MMSQPSAMSAGGAMQAGVNPSPAP---CONVTNPLEGSPSPISQ---667
Chop2..NGMS..GVVANVTPSAAGSMGMGNAGAAPQSPGMNCGRLSTNPFNAPPLSSQLGA676

(Seq ID No. 1) Chop1. ---PCISPTATPPATAAPAGAGSGEAFMIQQQLMSFNIPIN-THGK 712
(Seq ID No. 2) Chop2. ---EAGMGSMGGMGSMGSMGCMGCMGGGAGATQAGGNAEAFMIQQLMNEHPIKREICH 737

Fig. 1D (continued)

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....5...10....5...20....5...30....5...40
MDYGGALSAVGRELLFVTNPVVVNGSVLVPEDQCYCAGWI 40
ESRGTNGAQTASNVLQWLAAGFSILLIMFYAYQTWKSTCG 80
WEEIYVCAIEMVKVILEFFFEFKNPSMLYLATGHRVQWLR 120
YAEWLLTCPVILIRLSNLTGLSNDYSRRTMGLLVSDIGTI 160
VWGATSAMATGYVKVIFFCGLCYGANTFFHAAKAYIEGY 200
HTVPKGRRCRQVVTGMAWLFFVSWGMPILFILGPEGFGVL 240
SVYGSTVGHTIIDLMSKNCWGLLGHYLRVLIHEHILIHGD 280
IRKTTKLNIGGTEIEVETLVEDEAEAGAVNKGTKG (Seq ID No. 4) 315

Fig. 1E